

ENTERED
See page 6

0590
0606

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OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/989,339

DATE: 06/10/2002

TIME: 15:44:01

Input Set : A:\BB-1067USCNT SEQ LST corrected.txt

Output Set: N:\CRF3\06102002\I989339.raw

3 <110> APPLICANT: Falco, Saverio Carl
4 Famodu, Layo
5 Rafalski, Jan A.
6 Ramaker, Michael
7 Tarczynski, Mitchell C.
8 Thorpe, Catherine
10 <120> TITLE OF INVENTION: PLANT METHIONINE SYNTHASE GENE AND METHODS FOR INCREASING
THE
11 METHIONINE CONTENT OF THE SEEDS OF PLANTS
13 <130> FILE REFERENCE: BB-1067-B
C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/989,339
C--> 16 <141> CURRENT FILING DATE: 2002-05-31
18 <150> PRIOR APPLICATION NUMBER: 08/703,829
19 <151> PRIOR FILING DATE: 1996-08-27
21 <160> NUMBER OF SEQ ID NOS: 55
23 <170> SOFTWARE: Microsoft Office 97
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 2639
27 <212> TYPE: DNA
28 <213> ORGANISM: Zea mays
30 <400> SEQUENCE: 1
31 caccacccac ctcccactcc cagttcaccc cgtcgtcctc ggcgccadca ctccctcgtcc 60
32 ccgggcgcta ctccccgcct ccacgggtcca aggaaagatg gcgtcccata ttgttgata 120
33 ccctcgcagt ggccccaaaga gggagctcaa gtttgccttg gactctttct gggatgggaa 180
34 gagcagcgcc gaggatttgg agaaaagtgc cactgacctg aggtctagca tctggaagca 240
35 aatgtcagaa gctgggatca agtacattcc cagcaatacc tcgtcgtact acgaccaggt 300
36 tcttgatacc acggccatgc ttggcgctgt ccagagcgc tactcttgga ctggaggcga 360
37 gattggcttg agcacctact tctctatggc caggggaaat gccactgtcc ctgccatgga 420
38 gatgaccaag tggtttgata caaactacca ctttattgtc cctgaacttg gtccaagcac 480
39 caagttcaca tacgcttctc acaaggctgt ttctgagtag aaggaggcaa aggcgctcgg 540
40 cattgataca gtcccagtgc ttgttgacc agtctcatal ttgctcctct ctaagcctgc 600
41 caagggtgtg gagaaatctt tctctcttct ttcacttctt ggtagcatte ttcccatcta 660
42 caaggagggt gttgctgagc tgaaggcagc tgggtgctta tggattcagc ttgatgagcc 720
43 tacccttggt aaagaccttg atgtcacga attggccgca ttctcttcag catatgctga 780
44 actggagtea tcgttctctg gattgaatgt gcttatcgag acatacttcg ctgatattcc 840
45 tgctgagtc tacaagaccc tcacatcatt gactggtgtg actgcttacg gtttcgatct 900
46 tatccgtgga gccaaagacc ttgatcttat caggagcagc ttccctctg ggaagtaact 960
47 ctctcgtggt gttgtagatg gacgcaacat ttgggctgat gatcttgctg catctcttag 1020
48 cactcttcat tctcttgagg ctgttgctgg caaggacaaa cttgtggtgt caacctcctg 1080
49 ctactgatg cacaccgctg ttgacctgtt aaatgagact aagctggatg atgagattaa 1140
50 gtcactgctt gcatttgctg cccaaaaggt tgttgaggtt aatgcccttg ccaaggcttt 1200
51 ggcaggccaa aaggatgagg tctactttgc agccaatgct gctgctcagg cctcaaggag 1260
52 atcatcgccc aggggtgaaa acgaggaggt ccagaaggct gcagctgctt tgaggggagc 1320
53 tgaccaccgc cgttctacca ctgtttctgc tagattggat gctcagcaga aaaagctcaa 1380

RAW SEQUENCE LISTING

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54 ccttcctgtc cttcccacaa ccacaattgg ttcattccct cagactgtgg aactcaggag 1440
55 gggttcgccgt gaatacaagg caaagaagat caccgaggac gaatacatca gtgccatcaa 1500
56 ggaagaaatc agcaaggtcg tcaagatcca agaggagctt gacattgatg tgcttggtgca 1560
57 tggagagcca gagagaaatg acatggttga gtacttcggt gagcaattat ctgggttttgc 1620
58 gttcactgcc aacggatggg tgcaatccta tggatcacgc tgtgtgaagc caccattat 1680
59 ctacggtgat gtcagccggc cgaaccccat gactgttttc tggccaaga tggcacagag 1740
60 catgaccctc cgtcccatga agggaatggt gactggtccg gtcacaatcc tcaactggtc 1800
61 attcgtcagg aacgaccagc ctaggtttga gacatgctac caaatagctc ttgcaatcaa 1860
62 aaaggagggt gaggatcttg aggtctgtgg tattcagggtg atccagatcg atgaggcagc 1920
63 tctaaggagg ggtctgccac tacgcaagtc agagcatgca ttctacctgg actgggctgt 1980
64 ccactctttc aggatcacca actgcgaggc ccaggacacc acccagatcc acaccacat 2040
65 gtgctactcc aacttcaacg acatcatcca ctccatcatc gacatggatg ccgatgtgat 2100
66 cacgatcgag aactcccggt ctgacgagaa gctactgtcc gtcttccgtg aggggtgtgaa 2160
67 gtacggagct ggcattggcc ctgggtgtcta cgacatccac tctcctagga ttccctccac 2220
68 agaggagatc gcagaccgag tcgagaagat gctcgccgtg ttcgacacca acatcctctg 2280
69 ggtgaaccct gactgtggtc tcaagacacg caagtacacg gaggtcaagc ccgccctgac 2340
70 caacatggtc tcggccacca agctcatccg caccagctt tgttttgaat aatttgggtg 2400
71 tttgatagct gcatggtctg atagcgcgga atgagccagt tgttttgaat aatttgggtg 2460
72 ttaccccttg ttccatggtg ttagtggttag gttagcctct cattggtgag atacgccgtt 2520
73 tcaagatgtg ttctaagttt ggagtggtg ttttctttg ggctatgttt ctgggggtat 2580
74 gtgtgtgctt tggttataaa cagaaatgaa atatgcagtc ttccaattga aaaaaaaaaa 2639

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76 <210> SEQ ID NO: 2

77 <211> LENGTH: 765

78 <212> TYPE: PRT

79 <213> ORGANISM: Zea mays

81 <400> SEQUENCE: 2

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82 Met Ala Ser His Ile Val Gly Tyr Pro Arg Met Gly Pro Lys Arg Glu
83   1           5           10           15
85 Leu Lys Phe Ala Leu Glu Ser Phe Trp Asp Gly Lys Ser Ser Ala Glu
86           20           25           30
88 Asp Leu Glu Lys Val Ala Thr Asp Leu Arg Ser Ser Ile Trp Lys Gln
89           35           40           45
91 Met Ser Glu Ala Gly Ile Lys Tyr Ile Pro Ser Asn Thr Ser Ser Tyr
92           50           55           60
94 Tyr Asp Gln Val Leu Asp Thr Thr Ala Met Leu Gly Ala Val Pro Glu
95   65           70           75           80
97 Arg Tyr Ser Trp Thr Gly Gly Glu Ile Gly Leu Ser Thr Tyr Phe Ser
98           85           90           95
100 Met Ala Arg Gly Asn Ala Thr Val Pro Ala Met Glu Met Thr Lys Trp
101           100           105           110
103 Phe Asp Thr Asn Tyr His Phe Ile Val Pro Glu Leu Gly Pro Ser Thr
104           115           120           125
106 Lys Phe Thr Tyr Ala Ser His Lys Ala Val Ser Glu Tyr Lys Glu Ala
107           130           135           140
109 Lys Ala Leu Gly Ile Asp Thr Val Pro Val Leu Val Gly Pro Val Ser
110 145           150           155           160
112 Tyr Leu Leu Leu Ser Lys Pro Ala Lys Gly Val Glu Lys Ser Phe Ser
113           165           170           175
115 Leu Leu Ser Leu Leu Gly Ser Ile Leu Pro Ile Tyr Lys Glu Val Val

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 Output Set: N:\CRF3\06102002\I989339.raw

```

116          180          185          190
118 Ala Glu Leu Lys Ala Ala Gly Ala Ser Trp Ile Gln Leu Asp Glu Pro
119          195          200          205
121 Thr Leu Val Lys Asp Leu Asp Ala His Glu Leu Ala Ala Phe Ser Ser
122          210          215          220
124 Ala Tyr Ala Glu Leu Glu Ser Ser Phe Ser Gly Leu Asn Val Leu Ile
125 225          230          235          240
127 Glu Thr Tyr Phe Ala Asp Ile Pro Ala Glu Ser Tyr Lys Thr Leu Thr
128          245          250          255
130 Ser Leu Ser Gly Val Thr Ala Tyr Gly Phe Asp Leu Ile Arg Gly Ala
131          260          265          270
133 Lys Thr Leu Asp Leu Ile Arg Ser Ser Phe Pro Ser Gly Lys Tyr Leu
134          275          280          285
136 Phe Ala Gly Val Val Asp Gly Arg Asn Ile Trp Ala Asp Asp Leu Ala
137          290          295          300
139 Ala Ser Leu Ser Thr Leu His Ser Leu Glu Ala Val Ala Gly Lys Asp
140 305          310          315          320
142 Lys Leu Val Val Ser Thr Ser Cys Ser Leu Met His Thr Ala Val Asp
143          325          330          335
145 Leu Val Asn Glu Thr Lys Leu Asp Asp Glu Ile Lys Ser Trp Leu Ala
146          340          345          350
148 Phe Ala Ala Gln Lys Val Val Glu Val Asn Ala Leu Ala Lys Ala Leu
149          355          360          365
151 Ala Gly Gln Lys Asp Glu Val Tyr Phe Ala Ala Asn Ala Ala Ala Gln
152          370          375          380
154 Ala Ser Arg Arg Ser Ser Pro Arg Val Thr Asn Glu Glu Val Gln Lys
155 385          390          395          400
157 Ala Ala Ala Ala Leu Arg Gly Ser Asp His Arg Arg Ser Thr Thr Val
158          405          410          415
160 Ser Ala Arg Leu Asp Ala Gln Gln Lys Lys Leu Asn Leu Pro Val Leu
161          420          425          430
163 Pro Thr Thr Thr Ile Gly Ser Phe Pro Gln Thr Val Glu Leu Arg Arg
164          435          440          445
166 Val Arg Arg Glu Tyr Lys Ala Lys Lys Ile Thr Glu Asp Glu Tyr Ile
167          450          455          460
169 Ser Ala Ile Lys Glu Glu Ile Ser Lys Val Val Lys Ile Gln Glu Glu
170 465          470          475          480
172 Leu Asp Ile Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met
173          485          490          495
175 Val Glu Tyr Phe Gly Glu Gln Leu Ser Gly Phe Ala Phe Thr Ala Asn
176          500          505          510
178 Gly Trp Val Gln Ser Tyr Gly Ser Arg Cys Val Lys Pro Pro Ile Ile
179          515          520          525
181 Tyr Gly Asp Val Ser Arg Pro Asn Pro Met Thr Val Phe Trp Ser Lys
182          530          535          540
184 Met Ala Gln Ser Met Thr Pro Arg Pro Met Lys Gly Met Leu Thr Gly
185 545          550          555          560
187 Pro Val Thr Ile Leu Asn Trp Ser Phe Val Arg Asn Asp Gln Pro Arg
188          565          570          575

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 Output Set: N:\CRF3\06102002\I989339.raw

```

190 Phe Glu Thr Cys Tyr Gln Ile Ala Leu Ala Ile Lys Lys Glu Val Glu
191          580          585          590
193 Asp Leu Glu Ala Ala Gly Ile Gln Val Ile Gln Ile Asp Glu Ala Ala
194          595          600          605
196 Leu Arg Glu Gly Leu Pro Leu Arg Lys Ser Glu His Ala Phe Tyr Leu
197          610          615          620
199 Asp Trp Ala Val His Ser Phe Arg Ile Thr Asn Cys Gly Val Gln Asp
200 625          630          635          640
202 Thr Thr Gln Ile His Thr His Met Cys Tyr Ser Asn Phe Asn Asp Ile
203          645          650          655
205 Ile His Ser Ile Ile Asp Met Asp Ala Asp Val Ile Thr Ile Glu Asn
206          660          665          670
208 Ser Arg Ser Asp Glu Lys Leu Leu Ser Val Phe Arg Glu Gly Val Lys
209          675          680          685
211 Tyr Gly Ala Gly Ile Gly Pro Gly Val Tyr Asp Ile His Ser Pro Arg
212          690          695          700
214 Ile Pro Ser Thr Glu Glu Ile Ala Asp Arg Val Glu Lys Met Leu Ala
215 705          710          715          720
217 Val Phe Asp Thr Asn Ile Leu Trp Val Asn Pro Asp Cys Gly Leu Lys
218          725          730          735
220 Thr Arg Lys Tyr Thr Glu Val Lys Pro Ala Leu Thr Asn Met Val Ser
221          740          745          750
223 Ala Thr Lys Leu Ile Arg Thr Gln Leu Ala Ser Ala Lys
224          755          760          765
226 <210> SEQ ID NO: 3
227 <211> LENGTH: 2443
228 <212> TYPE: DNA
229 <213> ORGANISM: Glycine max
231 <220> FEATURE:
232 <221> NAME/KEY: unsure
233 <222> LOCATION: (460)
234 <223> OTHER INFORMATION: n = A, C, G, or T
236 <220> FEATURE:
237 <221> NAME/KEY: unsure
238 <222> LOCATION: (2398)
239 <223> OTHER INFORMATION: n = A, C, G, or T
241 <220> FEATURE:
242 <221> NAME/KEY: unsure
243 <222> LOCATION: (2442)
244 <223> OTHER INFORMATION: n = A, C, G, or T
246 <400> SEQUENCE: 3
247 ccctcagaag cgaagaagaa gccacagaga accagtctcc tactctctct caccacaag 60
248 aaaaatggca tctcacatcg ttggataccc ccgcatgggt cccaagagag agctcaagtt 120
249 cgctctcgag tctttctggg atggcaagag cagcgccgag gatttgcaga aggtggctgc 180
250 tgatctcagg tcatccatct ggaagcagat ggctggtgct gggatcaagt acatccccag 240
251 caacactttc tcgttctatg accagctgct cgacgccacc gccaccctcg gtgcggtccc 300
252 ccccaggtag ggctggaccg gcggcgagat tggattcgac acctacttct ccatggccag 360
253 aggtaatgct accgtgcctg ctatggagat gaccaagtgg ttcgacacca actaccactt 420
w--> 254 tattgtccct gaattgggcc ctgatgtgaa cttcacctan gcttctcaaa aggctgttga 480

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 Output Set: N:\CRF3\06102002\I989339.raw

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255 tgaatacaag gaggccaagg cgcttgaggt ggataccatt cccgtactcg ttggccctgt 540
256 tacatacttg ttgctctcca agcctgccaa gggagtcgag aaatcctttt ctctcctctc 600
257 tctccttccc aagggttcttg ctgtctacaa ggaagttatt gctgacctta aggcagctgg 660
258 tgcttcatgg attcaatttg atgagcctac ccttgctctg gaccttgaat ctcacaagtt 720
259 gcaagctttc actgaogcat atgcagaact tgcacctgct ttgtctgac tgaatgttct 780
260 tgttgagacc tactttgctg acatccctgc tgaggcgtac aagaccctca catctctgaa 840
261 tggcgtcaact gcatatgggt ttgatttggg ccgtggaacc catactcttg atttgatcaa 900
262 ggggtgattt cccagtggaa aatacctctt tgctggagtg gttgatggaa ggaacatctg 960
263 ggccaatgac cttgctgctt ctctcactac attgcagggt cttgagggca ttgtgggcaa 1020
264 agataagctt gttgtgtcca cctcctcctc cttctctcac actgctgttg atcttgtaa 1080
265 cgagaccaag ttggatgacg agatcaagtc atggctagca tttgctgcac aaaaaattgt 1140
266 tgaagttaac gcattggcta aggcattgtc tggcaacaag gatgtggcct tcttctctgc 1200
267 taatgctgca gctcaggctt caaggaagtc ctctccaaga gtgaccaacg aggctgttca 1260
268 gaaggctgct gctgcattga agggttcaga tcatcgccgt gcaacaaatg tcagtgccag 1320
269 actggatgct caacaaaaga agctcaacct tccaatcctt ccaaccacca ctattggatc 1380
270 cttccctcag actgtagaac tgaggagggg acgccgtgag ttcaaggcta acaagatctc 1440
271 cgaggaagag tatgttaagt caattaagga ggaaattcgc aaagtgttg aacttcaaga 1500
272 agagcttgat attgatgttc ttgttcatgg agaaccagag agaaatgata tggttgagta 1560
273 cttcgggtgag caattgtcag gctttgcctt cactgttaat ggggtgggtgc aatcctatgg 1620
274 ttcccgttgt gtgaagccac caatcatcta tgggtgatgt agccgcccaa agccaatgac 1680
275 tgtcttcttg tcatctctgg ctccagagctt taccagcgc ccaatgaagg gaatgcttac 1740
276 cggctcctgtt accattctca actggtcctt tgttagaaat gaccaaccta gatctgagac 1800
277 cacctaccag attgctttgg ctatcaagga cgaagtggag gaccttgaaa aggctggcat 1860
278 cactgttatc caaattgatg aagctgcttt gagagagggg ctgccactga ggaaatcaga 1920
279 acaagctcac tacttggact gggctgtcca tgccttcaga atcaccaatg ttgggtgtgca 1980
280 ggataccact cagatccaca cccacatgtg ctactccaac ttcaacgaca tcatccactc 2040
281 catcatcgac atggacgctg atgttatcac cattgagaac tctcgctccg atgagaagct 2100
282 cctgtcagtc ttccgtgaag gtgtgaagta tgggtgctgga attggccctg gtgtctatga 2160
283 catccactcc ccaagaatac caccaactga agaaatcgct gacagaatca ataagatgct 2220
284 tgcagtgtct gagaagaaca tcttgtgggt caaccctgac tgtgggtctca agaccgcaa 2280
285 gtacactgaa gtgaagccgc cctcacaaaa catggttgcc gcagcaaaac tcatccgcta 2340
W--> 286 cgaacttgcc aagtgaatgg tataagaaag tagaatctac aagttcaatg ggtccgcntt 2400
W--> 287 taaaatacac caaagaaaaa ttttcaaaat gggttgttca ana 2443
289 <210> SEQ ID NO: 4
290 <211> LENGTH: 763
291 <212> TYPE: PRT
292 <213> ORGANISM: Glycine max
294 <220> FEATURE:
295 <221> NAME/KEY: UNSURE
296 <222> LOCATION: (132)
297 <223> OTHER INFORMATION: Xaa = any amino acid
299 <400> SEQUENCE: 4
300 Met Ala Ser His Ile Val Gly Tyr Pro Arg Met Gly Pro Lys Arg Glu
301 1 5 10 15
303 Leu Lys Phe Ala Leu Glu Ser Phe Trp Asp Gly Lys Ser Ser Ala Glu
304 20 25 30
306 Asp Leu Gln Lys Val Ala Ala Asp Leu Arg Ser Ser Ile Trp Lys Gln
307 35 40 45
309 Met Ala Gly Ala Gly Ile Lys Tyr Ile Pro Ser Asn Thr Phe Ser Phe

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/989,339

DATE: 06/10/2002
TIME: 15:44:02

Input Set : A:\BB-1067USCNT SEQ LST corrected.txt
Output Set: N:\CRF3\06102002\I989339.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 460,2398,2442
Seq#:4; Xaa Pos. 132
Seq#:7; N Pos. 344,367,433,452,473,474
Seq#:8; Xaa Pos. 98,117,120
Seq#:9; N Pos. 219,254,300,319,331,335,338,348,350,360,413,416,424,428,440
Seq#:9; N Pos. 455,469,473,484,504,506,526,533,535,552,568,580,598,600,606
Seq#:9; N Pos. 613
Seq#:10; Xaa Pos. 8,72,73,84,100,106,110,112,116
Seq#:55; N Pos. 1461,1464,1465

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/989,339

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Input Set : A:\BB-1067USCNT SEQ LST corrected.txt
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L:15 M:270 C: Current Application Number differs, Replaced Application Number
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:420
L:286 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2340
L:287 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2400
L:324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:128
L:676 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:300
L:677 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:360
L:678 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:420
L:719 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:96
L:722 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:112
L:889 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:180
L:890 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:240
L:891 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:300
L:892 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:360
L:893 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:420
L:894 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:480
L:895 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:540
L:896 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:600
L:944 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:956 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:64
L:959 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:80
L:962 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:96
L:965 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:112
L:2148 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55 after pos.:1440